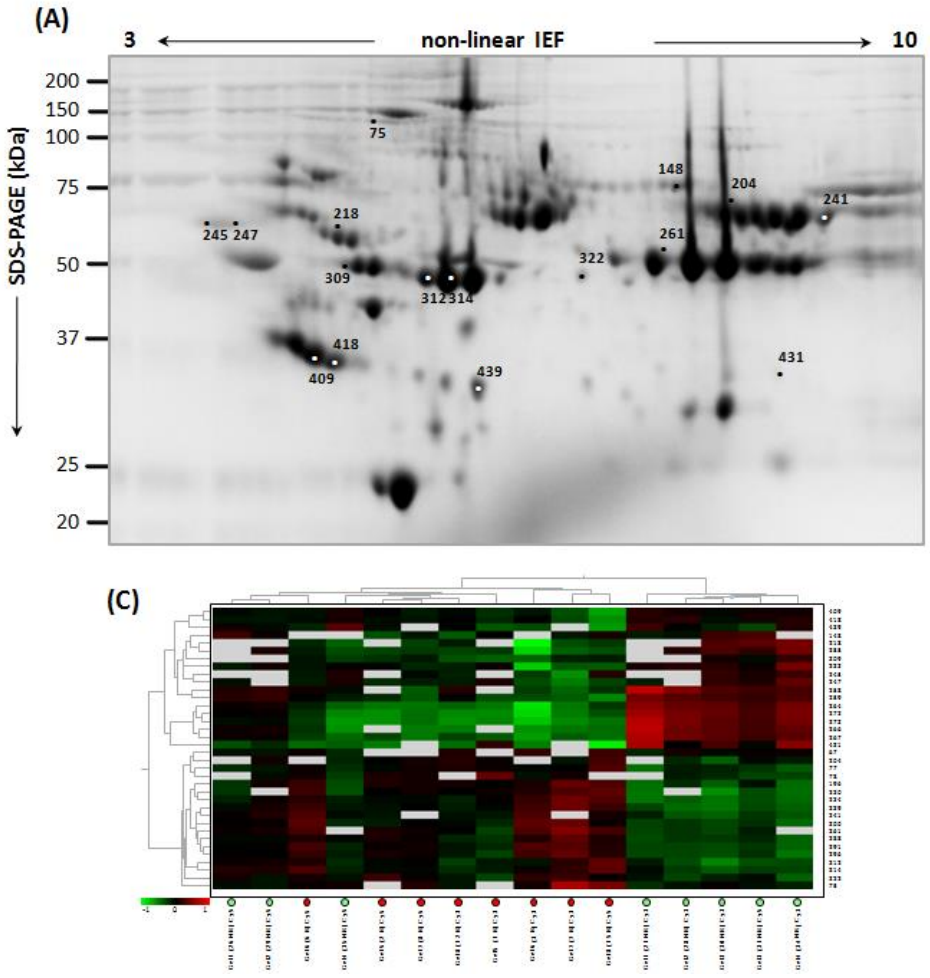

(B)

Spot nr.	Fold Δ	p-value
(a) up-regulated spots in 'relapsing, R' patients		
75	2.31	0.0248
261	2.04	0.0268
241	1.72	0.0366
312	1.68	0.0345
314	1.60	0.0496
204	1.53	0.0373
322	1.50	0.0485
(b) up-regulated spots in 'not relapsing, NR' patients		
218	-3.55	0.0493
431	-3.42	0.0252
439	-1.91	0.0292
247	-1.89	0.0142
245	-1.87	0.0387
148	-1.72	0.0390
309	-1.65	0.0498
409	-1.54	0.0161
418	-1.5	0.0218

Figure S1. Differential spots in two-dimensional proteome map of Hodgkin Lymphoma plasma samples of the 'explorative' cohort. (A) The numbers indicate 16 differentially expressed spots between 'relapsing' (R) and 'not relapsing' (NR) patient groups in the 'explorative' cohort, which were found adopting less stringent filter criteria (>50% of spot maps, Student's T-test $p<0.05$). In this protein map, differentially expressed spots found adopting more stringent filter criteria (>70% of spot maps, Student's T-test $p<0.01$) are not shown. (B) Details of the 16 differential spots. (C) Hierarchical clustering performed as 'Proteins - Spot maps' clustered the 16 differential spots depending on their expression profiles, and spots maps with similar overall protein expression were grouped together (as explained in §'Materials and methods').

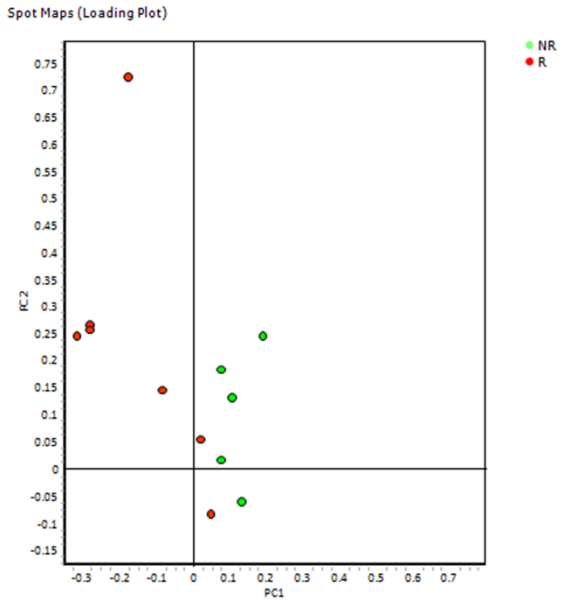

Figure S2. Principal component analysis of Hodgkin Lymphoma plasma samples of the 'validation' cohort. Spot Maps (Loading Plot) discriminated between 'relapsing' (R) and 'not relapsing' (NR) patient groups. Each circle represents a spot map corresponding to a single patient.

Table S1. Detailed clinicopathological characteristics of the 'explorative' cohort of patients affected by Hodgkin Lymphoma and showing either a favourable ('NR', not relapsing) or an unfavourable ('R', relapsing) response after treatment with the LH-2004 clinical trial [4]. Pathological and guidelines criteria to assess the relapse were drafted and discussed by AIEOP Organization [4].

Group	Patient nr.	Sex	Age at diagnosis	Histology[a]	Stage[b]	Sympthom[c]	Therapeutic Group
NR	1	M	13	Nodular sclerosis	2	A	2
	2	M	12	Nodular sclerosis	4	B	3
	3	M	16	Nodular sclerosis	4	B	3
	4	F	14	Nodular sclerosis	4	A	3
	5	F	13	Nodular sclerosis	2	A	2
	6	M	17	Not available	4	B	3
	7	F	15	Nodular sclerosis	2	A	1
	8	F	13	Nodular sclerosis	3	B	3
R	1	F	12	Mixed cellularity	4	A	3
	2	F	15	Not available	4	B	3
	3	M	13	Nodular sclerosis	2	B	3
	4	F	15	Not available	2	A	3
	5	M	15	Nodular sclerosis	2	A	3
	6	M	18	Nodular sclerosis	4	A	3
	7	M	9	Nodular sclerosis	3	A	3
	8	M	12	Nodular sclerosis	2	A	3

[a]histology according to [42]; [b]stage according to [43]; [c]A, absence of systemic symptoms; B, presence of systemic symptoms, according to [43]; [d]NR, absence of HL relapse within 3 years; R, relapsed HL within 3 years.

Table S2. Detailed clinicopathological characteristics of the 'validation' cohort of patients affected by Hodgkin Lymphoma and showing either a favourable ('NR', not relapsing) or an unfavourable ('R', relapsing) response after treatment with the LH-2004 clinical trial [4]. Pathological and guidelines criteria to assess the relapse were drafted and discussed by AIEOP Organization [4].

Group	Patient nr.	Sex	Age at diagnosis	Histology[a]	Stage[b]	Sympthom[c]	Therapeutic Group
NR	1	M	12	Nodular sclerosis	2	B	3
	2	F	16	Not available	3	B	3
	3	M	18	Nodular sclerosis	2	B	3
	4	F	14	Mixed cellularity	4	B	3
	5	F	11	Not available	3	B	3
	6	F	13	Mixed cellularity	3	A	3
R (nr=7)	1	M	18	Nodular sclerosis	4	A	3
	2	M	14	Nodular sclerosis	4	B	3
	3	M	12	Mixed cellularity	4	A	3
	4	M	13	Nodular sclerosis	2	B	3
	5	M	13	Mixed cellularity	3	A	3
	6	M	16	Not available	2	B	3
	7	M	15	Nodular sclerosis	2	A	3

[a]histology according to [42]; [b]stage according to [43]; [c]A, absence of systemic symptoms; B, presence of systemic symptoms, according to [42]; [d]NR, absence of HL relapse within 3 years; R, relapsed HL within 3 years.

Table S3. List of differentially expressed proteins of relapsing *versus* not-relapsing plasma collected from patients affected by Hodgkin Lymphoma belonging to the 'validation' cohort.

Spot nr.	MW(Da)/pI	Database	Accession	Protein annotation	Score	Matches	Seq.[a]	Seq. cov. %[b]	Fold △	*p*-value
(a) up-regulated spots (nr=2) in 'relapsing, R' patients										
403	56577/ 8.54	SwissProt	FIBB_HUMAN	fibrinogen β chain	84	6	3	7	1.67	0.017
	52655/8.76	NCBInr	gi|2765421	immunoglobulin kappa hea chain	52	8	5	10		
244	95656/ 5.70	NCBInr	gi|11761629	fibrinogen α chain	93	11	9	15	1.42	0.049
(b) up-regulated spots (nr=7) in 'not relapsing, NR' patients										
173	71317/ 5.92	SwissProt	ALBU_HUMAN	serum albumin	60	5	5	8	-4.03	0.00012
546	30132/ 7.59	NCBInr	1::gi|21669409	immunoglobulin kappa light chain VLJ region	29	2	2	10	-4.02	0.0068
56	52106/ 5.37	SwissProt	FIBG_HUMAN	fibrinogen γ chain	353	34	15	28	-2.87	0.0064
435	46878/ 5.37	SwissProt	A1AT_HUMAN	α-1-antitrypsin	59	4	4	8	-1.93	0.0083
202	71317/ 5.92	SwissProt	ALBU_HUMAN	serum albumin	52	8	13	13	-1.59	0.028
417	52106/ 5.37	SwissProt	FIBG_HUMAN	fibrinogen γ chain	408	42	18	33	-1.55	0.034
430	52106/ 5.37	SwissProt	FIBG_HUMAN	fibrinogen γ chain	390	42	18	36	-1.46	0.006

[a]Seq., sequences; [b]Seq. cov. %, percentage of sequence coverage.